FIG. 1A-1

FeB71.TAMU

```
ATGGGTCACGCAGCAAAGTGGAAAACACCACTACTGAAGCACCCATATCCCAAGCTCTTT 60
Met Gly His Ala Ala Lys Trp Lys Thr Pro Leu Leu Lys His Pro Tyr Pro Lys Leu Phe

CCGCTCTTGATGCTAGCTAGTCTTTTTTACTTCTGTTCAGGTATCATCCAGGTGAACAAG 120
Pro Leu Leu Met Leu Ala Ser Leu Phe Tyr Phe Cys Ser Gly Ile Ile Gln Val Asn Lys

ACAGTGGAAGAAGTAGCAGTACTATCCTGTGATTACAACATTTCCACCAAAGAACTGACG 180
Thr Val Glu Glu Val Ala Val Leu Ser Cys Asp Tyr Asn Ile Ser Thr Lys Glu Leu Thr

GAAATTCGAATCTATTGGCAAAAGGATGATGAAATGGTGTTGGCTGTCATGTCTGGCAAA 240
Glu Ile Arg Ile Tyr Trp Gln Lys Asp Asp Glu Met Val Leu Ala Val Met Ser Gly Lys

GTACAAGTGTGGCCCAAGTACAAGAACCGCACATTCACTGACGTCACCGATAACCACTCC 300
Val Gln Val Trp Pro Lys Tyr Lys Asn Arg Thr Phe Thr Asp Val Thr Asp Asn His Ser

ATTGTGATCATGGCTCTGCGCCTGTCAGACAATGGCAAATACACTTGTATTATTCAAAAG 360
Ile Val Ile Met Ala Leu Arg Leu Ser Asp Asn Gly Lys Tyr Thr Cys Ile Ile Gln Lys

ATTGAAAAAGGGTCTTACAAAGTGAAACACCTGACTTCGGTGATGTTATTGGTCAGAGCT 420
Ile Glu Lys Gly Ser Tyr Lys Val Lys His Leu Thr Ser Val Met Leu Leu Val Arg Ala

GACTTCCCTGTCCCTAGTATAACTGATCTTGGAAATCCATCTCATAACATCAAAAGGATA 480
Asp Phe Pro Val Pro Ser Ile Thr Asp Leu Gly Asn Pro Ser His Asn Ile Lys Arg Ile

ATGTGCTTAACTTCTGGAGGTTTTCCAAAGCCTCACCTCTCCTGGCTGGAAAATGAAGAA 540
Met Cys Leu Thr Ser Gly Gly Phe Pro Lys Pro His Leu Ser Trp Leu Glu Asn Glu Glu

GAATTAAATGCCATCAACACAACAGTTTCCCAAGATCCTGAAACTGAGCTCTACACTATT 600
Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu Thr Glu Leu Tyr Thr Ile

AGCAGTGAACTGGATTTCAATATGACAAACAACCATAGCTTCCTGTGTCTTGTCAAGTAT 660
Ser Ser Glu Leu Asp Phe Asn Met Thr Asn Asn His Ser Phe Leu Cys Leu Val Lys Tyr
```

FIG. 1A-2

GGAAACTTACTAGTATCACAGATCTTCAACTGGCAAAAATCAGAGCCACAGCCTTCTAAT 720
Gly Asn Leu Leu Val Ser Gln Ile Phe Asn Trp Gln Lys Ser Glu Pro Gln Pro Ser Asn

AATCAGCTCTGGATCATTATCCTGAGCTCAGTAGTAAGTGGGATTGTTGTGATCACTGCA 780
Asn Gln Leu Trp Ile Ile Ile Leu Ser Ser Val Val Ser Gly Ile Val Val Ile Thr Ala

CTTACCTTAAGATGCCTAGTCCACAGACCTGCTGCAAGGTGGAGACAAAGAGAAATGGGG 840
Leu Thr Leu Arg Cys Leu Val His Arg Pro Ala Ala Arg Trp Arg Gln Arg Glu Met Gly

AGAGCGCGGAAATGGAAAAGATCTCACCTGTCTACATAGATTCTGCAGAACCACTGTATG 900
Arg Ala Arg Lys Trp Lys Arg Ser His Leu Ser Thr

CAGAGCATCTGGAGGTAGCCTCTTTAGCTCTTCTCTACTAG 941

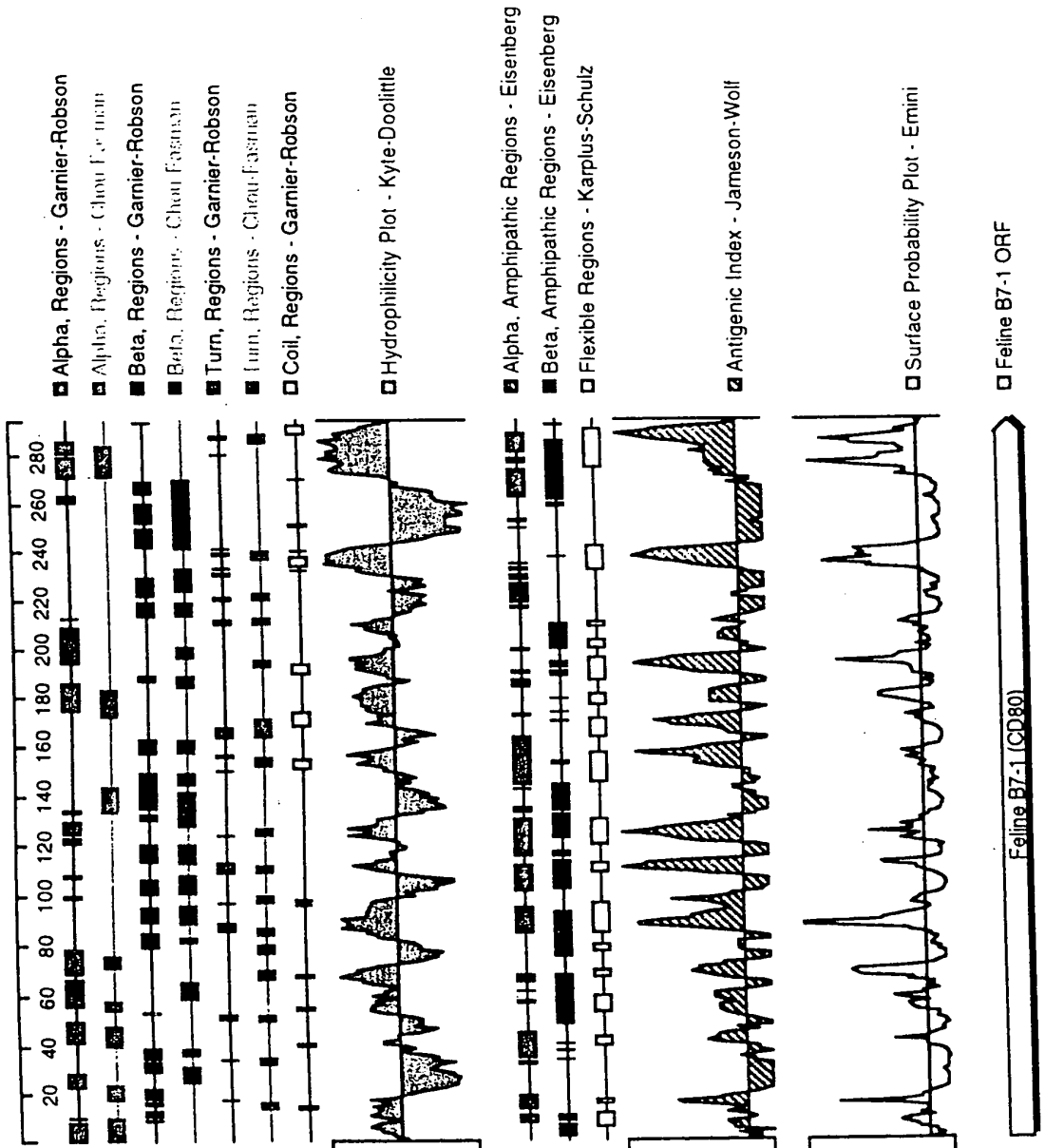

FIG. 1B

FIG. 2A-1

FeB71-SYNTRO

```
ATGGGTCACGCAGCAAAGTGGAAAACACCACTACTGAAGCACCCATATCCCAAGCTCTTT 60
Met Gly His Ala Ala Lys Trp Lys Thr Pro Leu Leu Lys His Pro Tyr Pro Lys Leu Phe

CCGCTCTTGATGCTAGCTAGTCTTTTTTACTTCTGTTCAGGTATCATCCAGGTGAACAAG 120
Pro Leu Leu Met Leu Ala Ser Leu Phe Tyr Phe Cys Ser Gly Ile Ile Gln Val Asn Lys

ACAGTGGAAGAAGTAGCAGTACTATCCTGTGATTACAACATTTCCACCAAAGAACTGACG 180
Thr Val Glu Glu Val Ala Val Leu Ser Cys Asp Tyr Asn Ile Ser Thr Lys Glu Leu Thr

GAAATTCGAATCTATTGGCAAAAGGATGATGAAATGGTGTTGGCTGTCATGTCTGGCAAA 240
Glu Ile Arg Ile Tyr Trp Gln Lys Asp Asp Glu Met Val Leu Ala Val Met Ser Gly Lys

GTACAAGTGTGGCCCAAGTACAAGAACCGCACATTCACTGACGTCACCGATAACCACTCC 300
Val Gln Val Trp Pro Lys Tyr Lys Asn Arg Thr Phe Thr Asp Val Thr Asp Asn His Ser

ATTGTGATCATGGCTCTGCGCCTGTCAGACAATGGCAAATACACTTGTATCATTCAAAAG 360
Ile Val Ile Met Ala Leu Arg Leu Ser Asp Asn Gly Lys Tyr Thr Cys Ile Ile Gln Lys

ATTGAAAAAGGGTCTTACAAAGTGAAACACCTGACTTCGGTGATGTTATTGGTCAGAGCT 420
Ile Glu Lys Gly Ser Tyr Lys Val Lys His Leu Thr Ser Val Met Leu Leu Val Arg Ala

GACTTCCCTGTCCCTAGTATAACTGATCTTGGAAATCCATCTCATAACATCAAAAGGATA 480
Asp Phe Pro Val Pro Ser Ile Thr Asp Leu Gly Asn Pro Ser His Asn Ile Lys Arg Ile

ATGTGCTTAACTTCTGGAGGTTTTCCAAAGCCTCACCTCTCCTGGCTGGAAAATGAAGAA 540
Met Cys Leu Thr Ser Gly Gly Phe Pro Lys Pro His Leu Ser Trp Leu Glu Asn Glu Glu

GAATTAAATGCCATCAACACAACAGTTTCCCAAGATCCTGAAACTGAGCTCTACACTATT 600
Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu Thr Glu Leu Tyr Thr Ile

AGCAGTGAACTGGATTTCAATATGACAAACAACCATAGCTTCCTGTGTCTTGTCAAGTAT 660
Ser Ser Glu Leu Asp Phe Asn Met Thr Asn Asn His Ser Phe Leu Cys Leu Val Lys Tyr
```

FIG. 2A-2

GGAAACTTAATAGTATCACAGATCTTCAACTGGCAAAAATCAGAGCCACAGCCTTCTAAT 720
Gly Asn Leu Ile Val Ser Gln Ile Phe Asn Trp Gln Lys Ser Glu Pro Gln Pro Ser Asn

AATCAGCTCTGGATCATTATCCTGAGCTCAGTAGTAAGTGGGATTGTTGTGATCACTGCA 780
Asn Gln Leu Trp Ile Ile Ile Leu Ser Ser Val Val Ser Gly Ile Val Val Ile Thr Ala

CTTACCTTAAGATGCCTAGTCCACAGACCTGCTGCAAGGTGGAGACAAAGAGAAATGGGG 840
Leu Thr Leu Arg Cys Leu Val His Arg Pro Ala Ala Arg Trp Arg Gln Arg Glu Met Gly

AGAGCGCGGAAATGGAAAAGATCTCACCTGTCTACATAG 879
Arg Ala Arg Lys Trp Lys Arg Ser His Leu Ser Thr

FIG. 2B

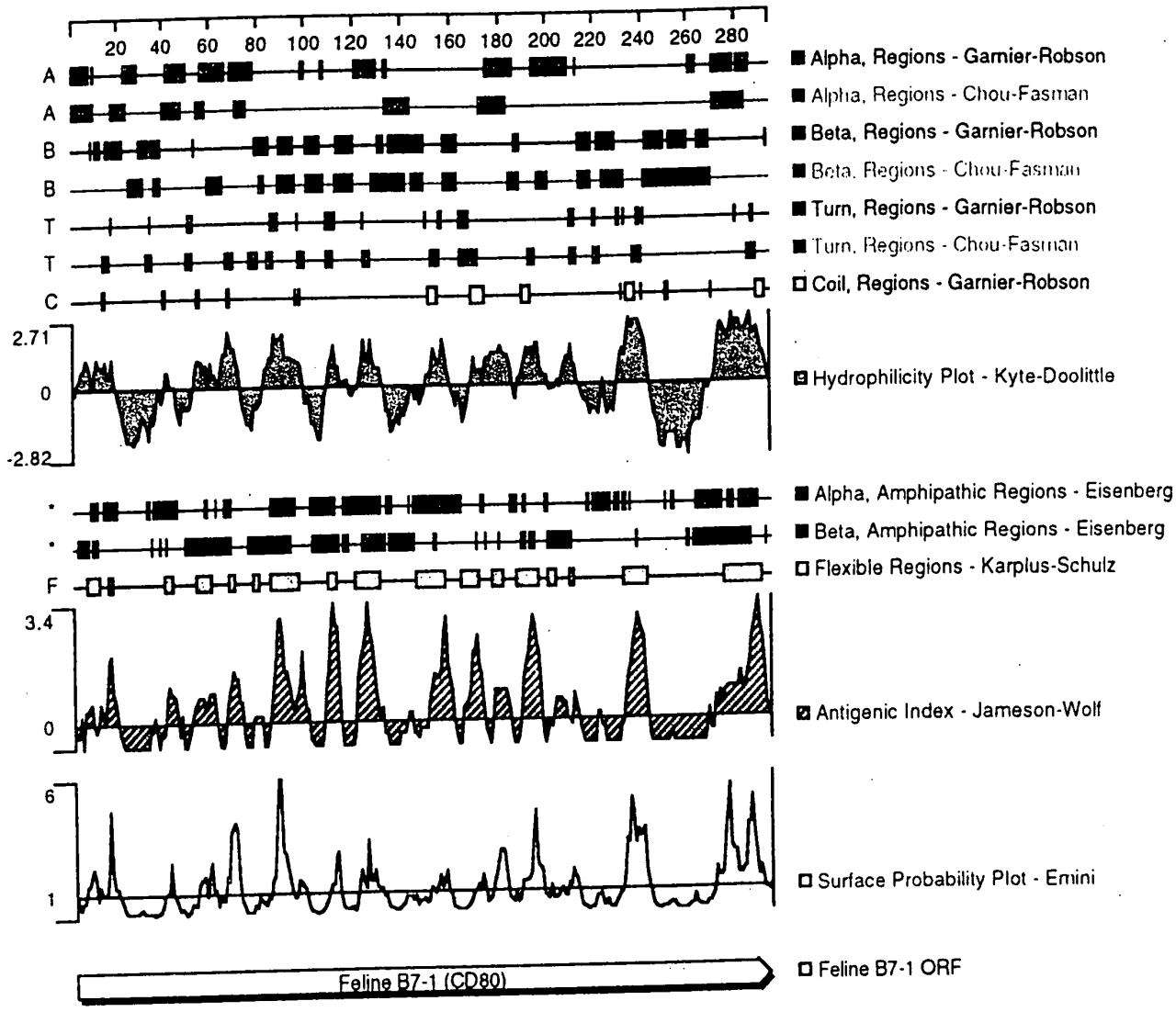

FIG. 3A-1

FeB72

```
GTTTCTGTGTTCCTCGGGAATGTCACTGAGCTTATACATCTGGTCTCTGGGAGCTGCAGT      60
GGATGGGCATTTGTGACAGCACTATGGGACTGAGTCACACTCTCCTTGTGATGGCCCTCC
  Met Gly Ile Cys Asp Ser Thr Met Gly Leu Ser His Thr Leu Leu Val Met Ala Leu   120

TGCTCTCTGGTGTTTCTTCCATGAAGAGTCAAGCATATTTCAACAAGACTGGAGAACTGC
Leu Leu Ser Gly Val Ser Ser Met Lys Ser Gln Ala Tyr Phe Asn Lys Thr Gly Glu Leu   180

CATGCCATTTTACAAACTCTCAAAACATAAGCCTGGATGAGCTGGTAGTATTTTGGCAGG
Pro Cys His Phe Thr Asn Ser Gln Asn Ile Ser Leu Asp Glu Leu Val Val Phe Trp Gln   240

ACCAGGATAAGCTGGTTCTGTATGAGATATTCAGAGGCAAAGAGAACCCTCAAAATGTTC
Asp Gln Asp Lys Leu Val Leu Tyr Glu Ile Phe Arg Gly Lys Glu Asn Pro Gln Asn Val   300

ATCTCAAATATAAGGGCCGTACAAGCTTTGACAAGGACAACTGGACCCTGAGACTCCACA
His Leu Lys Tyr Lys Gly Arg Thr Ser Phe Asp Lys Asp Asn Trp Thr Leu Arg Leu His   360

ATGTTCAGATCAAGGACAAGGGCACATATCACTGTTTCATTCATTATAAAGGGCCCAAAG
Asn Val Gln Ile Lys Asp Lys Gly Thr Tyr His Cys Phe Ile His Tyr Lys Gly Pro Lys   420

GACTAGTTCCCATGCACCAAATGAGTTCTGACCTATCAGTGCTTGCTAACTTCAGTCAAC
Gly Leu Val Pro Met His Gln Met Ser Ser Asp Leu Ser Val Leu Ala Asn Phe Ser Gln   480

CTGAAATAACAGTAACTTCTAATAGAACAGAAAATTCTGGCATCATAAATTTGACCTGCT
Pro Glu Ile Thr Val Thr Ser Asn Arg Thr Glu Asn Ser Gly Ile Ile Asn Leu Thr Cys   540

CATCTATACAAGGTTACCCAGAACCTAAGGAGATGTATTTTCAGCTAAACACTGAGAATT
Ser Ser Ile Gln Gly Tyr Pro Glu Pro Lys Glu Met Tyr Phe Gln Leu Asn Thr Glu Asn   600

CAACTACTAAGTATGATACTGTCATGAAGAAATCTCAAAATAATGTGACAGAACTGTACA
Ser Thr Thr Lys Tyr Asp Thr Val Met Lys Lys Ser Gln Asn Asn Val Thr Glu Leu Tyr   660

ACGTTTCTATCAGCTTGCCTTTTTCAGTCCCTGAAGCACACAATGTGAGCGTCTTTTGTG
Asn Val Ser Ile Ser Leu Pro Phe Ser Val Pro Glu Ala His Asn Val Ser Val Phe Cys   720

CCCTGAAACTGGAGACACTGGAGATGCTGCTCTCCCTACCTTTCAATATAGATGCACAAC
Ala Leu Lys Leu Glu Thr Leu Glu Met Leu Leu Ser Leu Pro Phe Asn Ile Asp Ala Gln   780

CTAAGGATAAAGACCCTGAACAAGGCCACTTCCTCTGGATTGCGGCTGTACTTGTAATGT
Pro Lys Asp Lys Asp Pro Glu Gln Gly His Phe Leu Trp Ile Ala Ala Val Leu Val Met   840

TTGTTGTTTTTTGTGGGATGGTGTCCTTTAAAACACTAAGGAAAAGGAAGAAGAAGCAGC
Phe Val Val Phe Cys Gly Met Val Ser Phe Lys Thr Leu Arg Lys Arg Lys Lys Lys Gln   900
```

FIG. 3A-2

CTGGCCCCTCTCATGAATGTGAAACCATCAAAAGGGAGAGAAAAGAGAGCAAACAGACCA 960
Pro Gly Pro Ser His Glu Cys Glu Thr Ile Lys Arg Glu Arg Lys Glu Ser Lys Gln Thr

ACGAAAGAGTACCATACCACGTACCTGAGAGATCTGATGAAGCCCAGTGTGTTAACATTT
Asn Glu Arg Val Pro Tyr His Val Pro Glu Arg Ser Asp Glu Ala Gln Cys Val Asn Ile 1020

TGAAGACAGCCTCAGGGGACAAAAATCAGTAGGAAAATGGTGGCTTGGCGTGCTGACAAT
Leu Lys Thr Ala Ser Gly Asp Lys Asn Gln • 1080

FIG. 3B Hydrophobicity plot: Feline CD86 (B7-2)

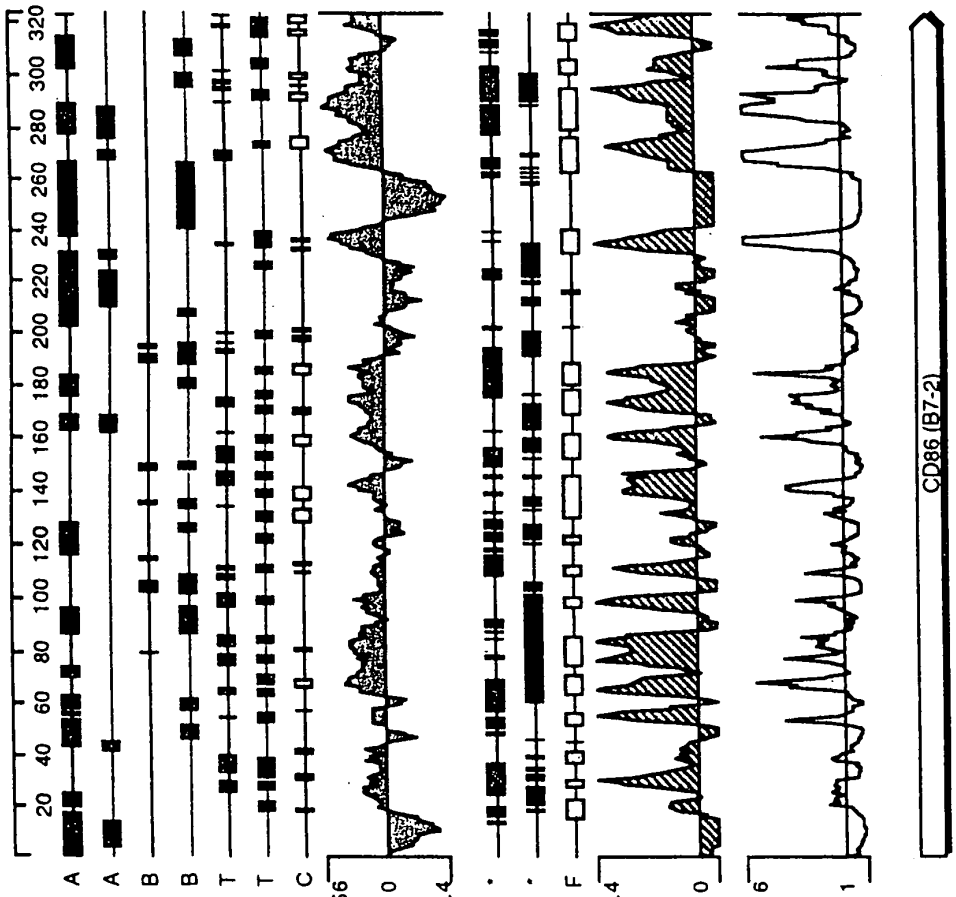

FIG. 4A

FeCD28

```
ATGATCCTCAGGCTGCTTCTGGCTCTCAACTTCTTCCCCTCAATTCAAGTAACAGAAAAC
Met Ile Leu Arg Leu Leu Leu Ala Leu Asn Phe Phe Pro Ser Ile Gln Val Thr Glu Asn 60

AAGATTTTGGTGAAGCAGTTGCCCAGGCTTGTGGTGTACAACAATGAGGTCAACCTTAGC 120
Lys Ile Leu Val Lys Gln Leu Pro Arg Leu Val Val Tyr Asn Asn Glu Val Asn Leu Ser

TGCAAGTACACTCACAACTTCTTCTCAAAGGAGTTCCGGGCATCCCTTTATAAGGGAGTA 180
Cys Lys Tyr Thr His Asn Phe Phe Ser Lys Glu Phe Arg Ala Ser Leu Tyr Lys Gly Val

GATAGTGCTGTGGAAGTCTGCGTTGTGAATGGAAATTACTCCCATCAGCCTCAGTTCTAC 240
Asp Ser Ala Val Glu Val Cys Val Val Asn Gly Asn Tyr Ser His Gln Pro Gln Phe Tyr

TCAAGTACAGGATTCGACTGTGATGGGAAATTGGGCAATGAAACAGTGACATTCTACCTC 300
Ser Ser Thr Gly Phe Asp Cys Asp Gly Lys Leu Gly Asn Glu Thr Val Thr Phe Tyr Leu

CGAAATTTGTTTGTTAACCAAACGGATATTTACTTCTGCAAAATTGAAGTCATGTATCCA 360
Arg Asn Leu Phe Val Asn Gln Thr Asp Ile Tyr Phe Cys Lys Ile Glu Val Met Tyr Pro

CCTCCTTACATAGACAATGAGAAGAGCAATGGGACCATTATCCACGTGAAAGAGAAACAT 420
Pro Pro Tyr Ile Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Glu Lys His

CTTTGTCCAGCTCAGCTGTCTCCTGAATCTTCCAAGCCATTTTGGGCACTGGTGGTGGTT 480
Leu Cys Pro Ala Gln Leu Ser Pro Glu Ser Ser Lys Pro Phe Trp Ala Leu Val Val Val

GGTGGAATCCTAGGTTTCTACAGCTTGCTAGCAACAGTGGCTCTTGGTGCTTGCTGGATG 540
Gly Gly Ile Leu Gly Phe Tyr Ser Leu Leu Ala Thr Val Ala Leu Gly Ala Cys Trp Met

AAGACCAAGAGGAGTAGGATCCTTCAGAGTGACTATATGAACATGACCCCCCGGAGGCCA 600
Lys Thr Lys Arg Ser Arg Ile Leu Gln Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro

GGGCCCACCCGAAGGCACTACCAACCTTACGCCCCAGCACGCGACTTTGCGGCATACCGT 660
Gly Pro Thr Arg Arg His Tyr Gln Pro Tyr Ala Pro Ala Arg Asp Phe Ala Ala Tyr Arg

TCCTGACATGGACCCCTATCCAGAAGCC 688
Ser
```

FIG. 4B Hydrophobicity Plot: CD28

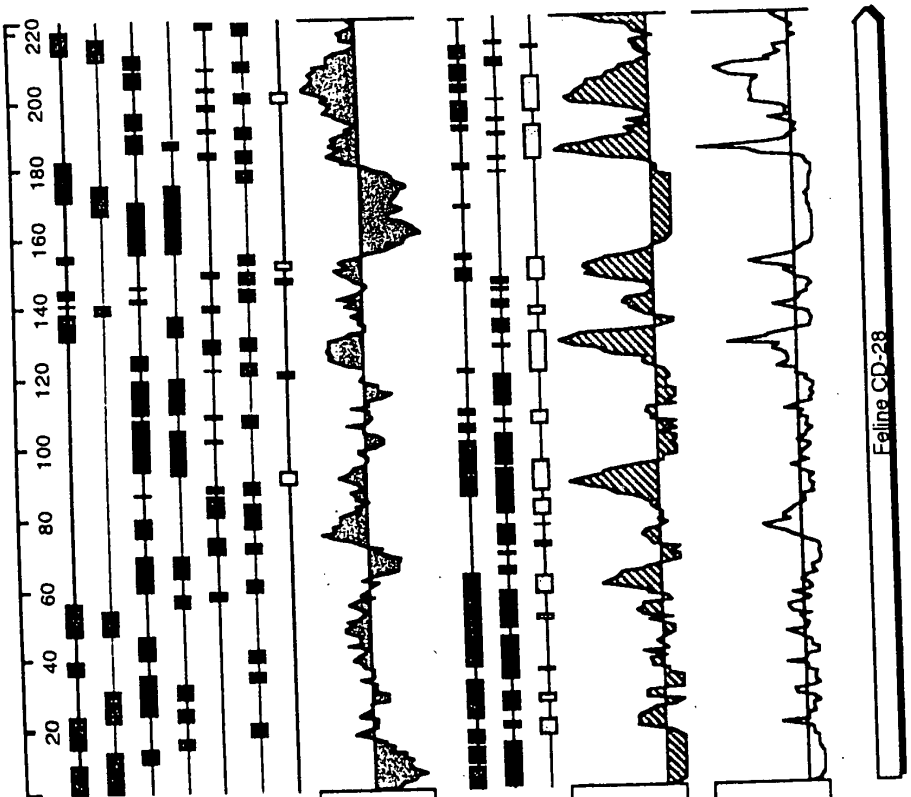

FIG. 5A

Fe CTLA4

```
AACCTGAACACTGCTCCCATAAAGCCATGGCTTGCTTTGGATTCCGGAGGCATGGGGCTC 60
                                Met Ala Cys Phe Gly Phe Arg Arg His Gly Ala

AGCTGGACCTGGCTTCTAGGACCTGGCCCTGCACTGCTCTGTTTTCTCTTCTCTTTATCC 120
Gln Leu Asp Leu Ala Ser Arg Thr Trp Pro Cys Thr Ala Leu Phe Ser Leu Leu Phe Ile

CCGTCTTCTCCAAAGGGATGCATGTGGCCCACCCTGCAGTGGTGCTGGCCAGCAGCCGAG 180
Pro Val Phe Ser Lys Gly Met His Val Ala His Pro Ala Val Val Leu Ala Ser Ser Arg

GTGTCGCCAGCTTCGTGTGTGAATATGGGTCTTCAGGCAATGCCGCCAAATTCCGAGTGA 240
Gly Val Ala Ser Phe Val Cys Glu Tyr Gly Ser Ser Gly Asn Ala Ala Lys Phe Arg Val

CTGTGCTGAGGCAAACTGGCAGCCAAATGACTGAAGTCTGTGCTGCGACATACACAGTGG 300
Thr Val Leu Arg Gln Thr Gly Ser Gln Met Thr Glu Val Cys Ala Ala Thr Tyr Thr Val

AGAATGAGTTGGCCTTCCTAAATGATTCCACCTGCACTGGCATCTCCAGCGGAAACAAAG 360
Glu Asn Glu Leu Ala Phe Leu Asn Asp Ser Thr Cys Thr Gly Ile Ser Ser Gly Asn Lys

TGAACCTCACCATCCAAGGGTTGAGGGCCATGGACACGGGACTCTACATCTGCAAGGTGG 420
Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val

AGCTCATGTACCCACCACCCTACTATGCAGGCATGGGCAATGGAACCCAGATTTATGTCA 480
Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Ala Gly Met Gly Asn Gly Thr Gln Ile Tyr Val

TCGATCCTGAACCTTGCCCAGATTCTGACTTCCTCCTCTGGATCCTCGCAGCAGTCAGTT 540
Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser

CAGGATTGTTTTTTTATAGCTTCCTTATCACAGCTGTTTCTTTGAGCAAAATGCTAAAGA 600
Ser Gly Leu Phe Phe Tyr Ser Phe Leu Ile Thr Ala Val Ser Leu Ser Lys Met Leu Lys

AAAGAAGCCCTCTTACTACAGGGGTCTATGTGAAAATGCCCCCAACAGAGCCAGAATGTG 660
Lys Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu Pro Glu Cys

AAAAGCAATTTCAGCCTTATTTTATTCCCATCAATTGACACACCGTTATGAAGAAGGAAG 720
Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn *

AACACTGTCCAATTTCTAAGAGCTGAGGC 749
```

FIG. 5B Hydrophobicity Plot: CTLA-4 (CD152)